

OM of: us-09-525-998A-2 for GenEmbl.* out_format: fls

Date: Apr 24, 2002 8:59 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:
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Search information block:

Query: us-09-525-998A.2

Query length: 455

Database: GenEmbl.*

Database sequences: 1472140

Database length: 341344837

Search time (sec): 2567.070090

score_list:

Sequence	Strd Oriq	ZScore	EScore Len	Documentation
gb_pat:A29098	2487.00	2815.33	1 50-148	A29098 Synthetic DNA for TNF
gb_pat:A21522	2487.00	2812.22	2 30-148	A21522 TNF alpha gene, 7/1991
gb_pat:HUMINFR	2487.00	2812.13	2 30-148	M33294 Human tumor necrosis fa
gb_pat:A26412	2487.00	2812.04	2 30-148	A26412 cDNA for (55K5 TNF-BF)
gb_pat:HUMINFR	2487.00	2812.04	2 30-148	M8286 Homo sapiens tumor necr
gb_pat:HUMINFR	2487.00	2811.84	2 40-148	M3121 Human tumor necrosis fa
gb_pat:A096330	2487.00	2811.86	2 40-148	A096330 Sequence 1 from patent
gb_pat:HUMINFR	2487.00	2811.86	2 40-148	X5313 H.sapiens TNF R mRNA fr
gb_pat:A43873	2487.00	2811.81	2 40-148	A43873 Sequence 1 from patent
gb_pat:A27878	2487.00	2811.81	2 40-148	A27878 Sequence 7 from patent
gb_pat:A29041076	2487.00	2811.81	2 40-148	A29041076 Sequence 1 from patent
gb_pat:A64751	2487.00	2811.81	2 40-148	A64751 Sequence 1 from patent
gb_pat:A19907	2487.00	2811.81	2 40-148	A19907 Synthetic nucleotide se
gb_pat:A210410	2487.00	2811.72	2 40-148	B2910140 Homo sapiens, tumor i
gb_pat:A43805	2482.00	2808.55	4 70-148	A43805 Sequence 24 from patent
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gb_pat:HUMINFR	2444.00	2764.54	1 20-148	M60275 Human tumor necrosis fa
gb_pat:A29104	2453.00	2763.34	3 40-122	A29103 H.sapiens mRNA for TNF
gb_pat:A051103	1801.50	2045.10	4 40-105	A051103 Felis catus TNFR 1 mR
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gb_pat:A43808	1512.00	1277.18	7 30-63	AC02527 Synthetic nucleotide seq
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seq_documentation_block: 2062 bf mpna PAT 26-JUL-1994

Locus: A21522

DEFINITION TNF alpha gene.

ACCESSION A21522

VERSION A21522.1 GI:579599

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates, Catarrhini, Hominiidae; Homo.

REFERENCE 1 (bases 1 to 2062)

AUTHORS

JOURNAL

FEATURES

source

gene

CDS

Location/Qualifiers

1..2062

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34 euGlyAspArgGluLysArgAspSerValCysProGlnGlyLysTyrIle 50
255 TAGCGGACACGGCAGAACACAGATACGTGCTGTCCTCCCAAGCAAAATAATC 304
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DEFINITION Sequence 1 from patent US 6007995.
ACCESSION AR096330
VERSION    AR096330.1  GI:10025045
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.

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REFERENCE
  1 (bases 1 to 2161)
AUTHORS   Baker,B.F. and Cowser,L.M.
TITLE      Antisense inhibition of TNF $\alpha$  expression
JOURNAL    Patent: US 6007995-A 1 28-DEC-1999;
FEATURES   location/qualifiers
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DEFINITION Sequence 1 from Patent EP0657536.
ACCESSION A43873
VERSION A43873.1 GI:2299022
KEYWORDS
SOURCE
  UNIDENTIFIED
  ORGANISM
  UNIDENTIFIED
  UNCLASSIFIED
REFERENCE
  1 (bases 1 to 2175)
  Wallach,D., Brackebusch,C., Variolomeev,E. and Balkin,M.
  Proteases capable of shedding the soluble TNF receptor and INF- $\gamma$ 
  derived peptides and antibodies against the proteases inhibiting
  the shedding
JOURNAL Patent: EP 0657536-A 1 14-JUN-1995;
  YEDA RES & DEV (IL)
COMMENT
  other publication ZA 9407962 951121
  other publication JP 7194376 950801
  other publication AU 7574294 950504
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ACCESSION BC010140

VERSION BC010140.1 GI:14603367

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ORGANISM Homo sapiens

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1. Alvarez, J. (1994)

Strausberg, R.

Direct Submission

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

Contact: MGC help desk

Email: mgc@ncbi.nlm.nih.gov

Tissue Procurement: APOC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (IMAGE)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Gaithersburg, Maryland

Web Site: <http://www.ncbi.nlm.nih.gov>

Contact: misc@ncbi.nlm.nih.gov

Shvachenko, Y., Wetherby, K.D., Beckstrom-Sterbert, S.M.,

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McDowell, J., Pearson, R., Snyder, R., Stadtrupp, S., Thomas, P.J.,

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Zhang, L.H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium web site: <http://image.llnl.gov>

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This clone was selected for full length sequencing because it

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334 LeProAsnProLeuGlnIleYsTrpGluAspSerAlaHisIleYsProGlnSer 350
|||||
1241 TCTTAAATATATATATATATATATATATATATATATATATATATAT 1290
351 LeuAspThrAspAspProAlaThrLeuTyrAlaValValGluAsnValPr 367
|||||
1291 CTACACACTGATATATATATATATATATATATATATATATATATATAT 1340
367 oProLeuArgTrpIleYsGluPheValArgArgLeuGlyLeuSerAspHisG 384
|||||
1341 CCGGTGTGATTTSSAAATATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 1390
384 IleIleAspArgLeuGluLeuGlnAsnGlyArgCysLeuArgGluAlaGln 400
|||||
1391 AGATTCATATATATATATATATATATATATATATATATATATATATAT 1440
401 TyrSerMetLeuAlaThrTrpArgArgArgThrProArgArgGluAlaTh 417
|||||
1441 TACACATATATATATATATATATATATATATATATATATATATATAT 1490
417 rLeuGluLeuLeuGlyArgValLeuLeuArgAspMetAspLeuGlyCysL 434
|||||
1491 GGTGATATATATATATATATATATATATATATATATATATATATATAT 1540
434 eUGluAspIleGluAlaIleCysGlyIleProAlaIleLeuProProAla 450
|||||
1541 TGGAGGATATATATATATATATATATATATATATATATATATATATAT 1590
451 ProSerLeuLeuArg 455
|||||
1591 CCCAGTCTCTCTCAGA 1605

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